

## Exhibit X



## Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

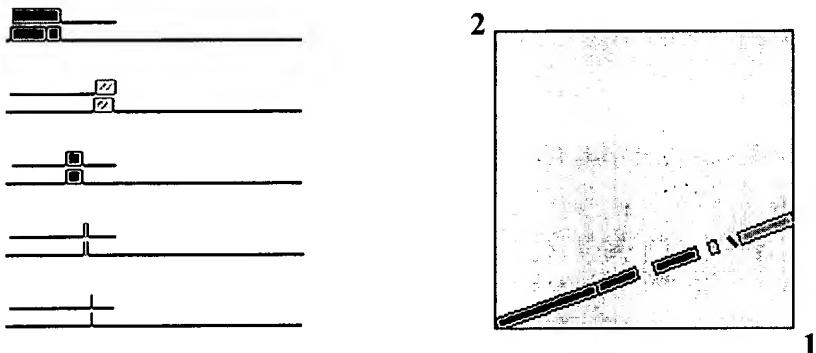
x\_dropoff: 50 expect: 10.000 wordsize: 11 Filter  View option StandardMasking character option X for protein, n for nucleotide  Masking color option Black  Show CDS translation Align

Sequence 1: gi|4454551|gb|AF113003.1|AF113003 SEQ ID NO:4

Length = 3094 (1 .. 3094)

Sequence 2: gi|4559297|gb|AF125672.1|AF125672

Length = 8686 (1 .. 8686)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.



Score = 2680 bits (1394), Expect = 0.0  
 Identities = 1465/1480 (98%), Gaps = 3/1480 (0%)  
 Strand=Plus/Plus

Query 1	CATGTCGGGCTCCACACAGCTTGTGGCACAGACGTGGAGGCCACTGAGCCCCGCTACCC	60
Sbjct 156	CATGTCGGGCTCCACACAGCCTGTGGCACAGACGTGGAGGCCACTGAGCCCCGCTACCC	215
Query 61	GCCCCACAGCCTTCCTACCCAGTGCAGATGCCGGACGCACACGGACGTGGCTCCT	120
Sbjct 216	GCCCCACAGCCTTCCTACCCAGTGCAGATGCCGGACGCACACGGACGTGGCTCCT	275
Query 121	GGAGTACCAGCACCCTCCCGACTATGCCTCCCACCTGTCGCCGGCTCCATCATCCA	180

Sbjct	276	GGAGTACCAAGCACCCTCCCGCGACTATGCCTCCACCTGTCGCCCGGCTCCATCATCCA	335
Query	181	GCCCGAGCGCGGGAGGCCCTCCCTGCTGTCTGAGTCCAGCCCAGGAATGAACGGTCCCA	240
Sbjct	336	GCCCGAGCGCGGGAGGCCCTCCCTGCTGTCTGAGTCCAGCCCAGGAATGAACGGTCCCA	395
Query	241	GGAGCTCACCTGCGGCCAGAGTCCACTCATACCTGCCAGCTGGGAAGTCAGAGAT	300
Sbjct	396	GGAGCTCACCTGCGGCCAGAGTCCACTCATACCTGCCAGCTGGGAAGTCAGAGAT	455
Query	301	GGAGTTCATTGAAAGCAAGCGCCCTCGGCTAGAGCTGCTGCCTGACCCCTGCTGCGACC	360
Sbjct	456	GGAGTTCATTGAAAGCAAGCGCCCTCGGCTAGAGCTGCTGCCTGACCCCTGCTGCGACC	515
Query	361	GTCACCCCTGCTGGCACGGGACGGCTGCGGATCTGAAGACCTCACCAAGGACCGTAG	420
Sbjct	516	GTCACCCCTGCTGGCACGGGACGGCTGCGGATCTGAAGACCTCACCAAGGACCGTAG	575
Query	421	CCTGACGGCAAGCTGGAACCGGTGTCTnnnnnnnnnnnnnGCACACTGACCTGAGCT	480
Sbjct	576	CCTGACGGCAAGCTGGAACCGGTGTCTCCCCCAGCCCCCGCACACTGACCTGAGCT	635
Query	481	GGAGCTGGTGCCACGGCTGTCCAAGGAGGAGCTGATCCAGAACATGGACCGCGTGG	540
Sbjct	636	GGAGCTGGTGCCACGGCTGTCCAAGGAGGAGCTGATCCAGAACATGGACCGCGTGG	695
Query	541	CCGAGAGATCACCATGGTAGAGCAGCAGATCTTAAGCTGAAGAAGAACAGCAACAGCT	600
Sbjct	696	CCGAGAGATCACCATGGTAGAGCAGCAGATCTTAAGCTGAAGAAGAACAGCAACAGCT	755
Query	601	GGAGGAGGAGGCTGCCAACGCCCGAGCCTGAGAACGCCGTGTCACCGCCGCCATCGA	660
Sbjct	756	GGAGGAGGAGGCTGCCAACGCCCGAGCCTGAGAACGCCGTGTCACCGCCGCCATCGA	815
Query	661	GTCGAAGCACCGCAGCCTGGCAGATCATCTACGACGAGAACCGGAAGAAGGCTGAAGC	720
Sbjct	816	GTCGAAGCACCGCAGCCTGGCAGATCATCTACGACGAGAACCGGAAGAAGGCTGAAGC	875
Query	721	TGCACATCGGATTCTGGAAGGCCTGGGCCAGGTGGAGCTGCCGTGTACAACCAGCC	780
Sbjct	876	TGCACATCGGATTCTGGAAGGCCTGGGCCAGGTGGAGCTGCCGTGTACAACCAGCC	935
Query	781	CTCGACACCGGCACTATGAGAACATCAAATAAACAGGCGATGCCAGAACGCT	840
Sbjct	936	CTCGACACCGGCACTATGAGAACATCAAATAAACAGGCGATGCCAGAACGCT	995
Query	841	AATCTTGTACTTCAAGAGGAGGAATCACGCTCGAACATGGAGCAGAACGAGTTCTGCCA	900
Sbjct	996	AATCTTGTACTTCAAGAGGAGGAATCACGCTCGAACATGGAGCAGAACGAGTTCTGCCA	1055
Query	901	GCGCTATGACCAGCTCATGGAGGCCTTGGhnnnnnnGGTGGAGGCCATGCCAAACACC	960
Sbjct	1056	GCGCTATGACCAGCTCATGGAGGCCTGGAGAACAGGTGGAGCGCATGCCAGAACACC	1115
Query	961	GCGCCGGCGGCCAAGGAGAGCAAGGTGCGCGAGTACTACGAAAAGCAGTCCCTGAGAT	1020
Sbjct	1116	CGGGCGGCCAGGCCAAGGAGAGCAAGGTTCGCGAGTACTACGAGAACAGCAGTCCCTGAGAT	1175
Query	1021	CCGCAAGCAGCGCGAGCTGCAGGAGCGCATGCCAGAGCAGGGTGGCCAGCGGGCAGTGG	1080

Sbjct	1176	CCGCAAGCAGCGCAGCTGCAGGAGCGCATGCAG---AGGGTGGGCCAGCGGGGCAGTGG	1232
Query	1081	GCTGTCCATGTCGGCCGCCGCAGCGAGCACGAGGTGTCAGAGATCATCGATGGCCTCTC 	1140
Sbjct	1233	GCTGTCCATGTCGCCGCCGCAGCGAGCACGAGGTGTCAGAGATCATCGATGGCCTCTC 	1292
Query	1141	AGAGCAGGAGAACCTGGAGAACGCAGATGCCAGCTGGCGTGATCCGCCATGCTGTA 	1200
Sbjct	1293	AGAGCAGGAGAACCTGGAGAACGCAGATGCCAGCTGGCGTGATCCGCCATGCTGTA 	1352
Query	1201	CGACGCTGACCAGCAGCGCATCAAGTTCATCAACATGAACGGCTTATGGCGACCCAT 	1260
Sbjct	1353	CGACGCTGACCAGCAGCGCATCAAGTTCATCAACATGAACGGCTTATGGCGACCCAT 	1412
Query	1261	GAAGGTGTACAAAGACCGCCAGGTATGAACATGTGGAGTGAGCAGGAGAAGGAGACCTT 	1320
Sbjct	1413	GAAGGTGTACAAAGACCGCCAGGTATGAACATGTGGAGTGAGCAGGAGAAGGAGACCTT 	1472
Query	1321	CCGGGAGAAGTCATGCAGCATCCCAAGAACTTGGCCTGATCGCATCATTCTGGAGAG 	1380
Sbjct	1473	CCGGGAGAAGTCATGCAGCATCCCAAGAACTTGGCCTGATCGCATCATTCTGGAGAG 	1532
Query	1381	GAAGACAGTGGCTGAGTGCCTCTATTACTACCTGACTAAGAAGAATGAGAACTATAA 	1440
Sbjct	1533	GAAGACAGTGGCTGAGTGCCTCTATTACTACCTGACTAAGAAGAATGAGAACTATAA 	1592
Query	1441	GAGCCTGGTGAGACGGAGCTATCGCGCCGCGCAAGAGC 1480 	
Sbjct	1593	GAGCCTGGTGAGACGGAGCTATCGCGCCGCGCAAGAGC 1632 	

Score = 1013 bits (527), Expect = 0.0  
Identities = 561/564 (99%), Gaps = 0/564 (0%)  
Strand=Plus/Plus

Query	2531	AAGCCCCCGCGCTGAGGAGCTGGCAGTGGACACAGGGAAAGGCCGAGGAGCCGTCAAG 	2590
Sbjct	2632	AAGCCCCCGCGCTGAGGAGCTGGCAGTGGACACAGGGAAAGGCCGAGGAGCCGTCAAG	2691
Query	2591	AGCGAGTGCACGGAGGAAGCCGAGGAGGGGCCAAGGGCAAGGACGCCGAGGCCGCT 	2650
Sbjct	2692	AGCGAGTGCACGGAGGAAGCCGAGGAGGGGCCCGCCAAGGGCAAGGACGCCGAGGCCGCT	2751
Query	2651	GAGGCCACGGCCGAGGGGGCGCTCAAGGCAGAGAAGAAGGAGGGCGGGAGCGGCAGGCC 	2710
Sbjct	2752	GAGGCCACGGCCGAGAGGGCGCTCAAGGCAGAGAAGAAGGAGGGCGGGAGCGGCAGGCC	2811
Query	2711	ACCACTGCCAAGAGCTCGGGGCCCCCCCAGGACAGCGACTCCAGTGCTACCTGCAGTGCA 	2770
Sbjct	2812	ACCACTGCCAAGAGCTCGGGGCCCCCCCAGGACAGCGACTCCAGTGCCACCTGCAGTGCA	2871
Query	2771	GACGAGGTGGATGAGGCCGAGGGCGGGCAGAACAGAACCGGCTGCTGTCCCCAAGGCCAGC 	2830
Sbjct	2872	GACGAGGTGGATGAGGCCGAGGGCGGGCAGAACAGAACCGGCTGCTGTCCCCAAGGCCAGC	2931

Query	2831	CTCCTCACCCGACTGGCGACCCCCGGCCAATGCCTCACCCAGAACGCCACTGGACCTG 	2890
Sbjct	2932	CTCCTCACCCGACTGGCGACCCCCGGCCAATGCCTCACCCAGAACGCCACTGGACCTG 	2991
Query	2891	AAGCAGCTGAAGCAGCGAGCGGCTGCCATnnnnnnnnATCCAGGTACCAAAGTCCATGAG 	2950
Sbjct	2992	AAGCAGCTGAAGCAGCGAGCGGCTGCCATCCCCCATCCAGGTACCAAAGTCCATGAG 	3051
Query	2951	nnnnnnnnGGGAGGACGCAGCTCCCACCAAGCCAGCTCCCCAGCCCCACCGCCACCGCAA 	3010
Sbjct	3052	CCCCCCCCGGGAGGACGCAGCTCCCACCAAGCCAGCTCCCCAGCCCCACCGCCACCGCAA 	3111
Query	3011	AACCTGCAGCCGGAGAGCGACGCCCTCAGCAGCCTGGCAGCAGCCCCGGGCAAGAGC 	3070
Sbjct	3112	AACCTGCAGCCGGAGAGCGACGCCCTCAGCAGCCTGGCAGCAGCCCCGGGCAAGAGC 	3171
Query	3071	AGGAGCCCGGCACCCCCCGCCGAC 3094 	
Sbjct	3172	AGGAGCCCGGCACCCCCCGCCGAC 3195	



Score = 898 bits (467), Expect = 0.0  
 Identities = 467/467 (100%), Gaps = 0/467 (0%)  
 Strand=Plus/Plus

Query	1633	CCTCCTCAAGGAGAACAGACGACACCTCAGGGGAGGACAACGACGAGAACGGAGGCTGT 	1692
Sbjct	1785	CCTCCTCAAGGAGAACAGACGACACCTCAGGGGAGGACAACGACGAGAACGGAGGCTGT 	1844
Query	1693	GGCCTCAAAGGCCGAAACTGCCAACAGCCAGGGAAAGACGCAAAGGCCGATCACCCG 	1752
Sbjct	1845	GGCCTCAAAGGCCGAAACTGCCAACAGCCAGGGAAAGACGCAAAGGCCGATCACCCG 	1904
Query	1753	CTCAATGGCTAATGAGGCCAACAGCGAGGAGGCCATCACCCCCAGCAGAGCGCCGAGCT 	1812
Sbjct	1905	CTCAATGGCTAATGAGGCCAACAGCGAGGAGGCCATCACCCCCAGCAGAGCGCCGAGCT 	1964
Query	1813	GGCCTCCATGGAGCTGAATGAGAGTTCTCGCTGGACAGAACAGCAA 	1872
Sbjct	1965	GGCCTCCATGGAGCTGAATGAGAGTTCTCGCTGGACAGAACAGCAA 	2024
Query	1873	GAAAGGTCTCTGGAACACGGCCGCAACTGGTCGGCATGCCGGATGGTGGCTCAA 	1932
Sbjct	2025	GAAAGGTCTCTGGAACACGGCCGCAACTGGTCGGCATGCCGGATGGTGGCTCAA 	2084
Query	1933	GACTGTGCGAGTGTAAAGAACTTCTACTTCAACTACAAGAACGGCAGAACCTCGATGA 	1992
Sbjct	2085	GACTGTGCGAGTGTAAAGAACTTCTACTTCAACTACAAGAACGGCAGAACCTCGATGA 	2144
Query	1993	GATCTTGCAGCAGCACAGCTGAAGATGGAGAACGGAGAGAACGCCGGAGGAAGAA 	2052
Sbjct	2145	GATCTTGCAGCAGCACAGCTGAAGATGGAGAACGGAGAGAACGCCGGAGGAAGAA 	2204
Query	2053	GAAAGGCCGGCGGCCAGCGAGGCTGCATTCCGCCGTGG 2099	

Sbjct 2205 GAAAGCGCCGGCGGCAGCGAGGAGGCTGCATTCCCGCCCGTGG 2251



Score = 154 bits (80), Expect = 2e-33  
Identities = 80/80 (100%), Gaps = 0/80 (0%)  
Strand=Plus/Plus

Query 2218 AGCCACTGTCAACAAACAGCTCAGACACCGAGAGCATCCCCTCTCCTCACACTGAGGCCGC 2277

Sbjct 2319 AGCCACTGTCAACAAACAGCTCAGACACCGAGAGCATCCCCTCTCCTCACACTGAGGCCGC 2378

Query 2278 CAAGGACACAGGGCAGAATG 2297

Sbjct 2379 CAAGGACACAGGGCAGAATG 2398



Score = 48.8 bits (25), Expect = 0.12  
Identities = 27/28 (96%), Gaps = 0/28 (0%)  
Strand=Plus/Plus

Query 2444 CCCTCTGCACCTCCTCCTGTGGTCCCCA 2471

Sbjct 2545 CCCTCTTCACCTCCTCCTGTGGTCCCCA 2572

CPU time: 0.05 user secs. 0.02 sys. secs 0.07 total secs.

Lambda K H  
1.33 0.621 1.12

Gapped

Lambda K H  
1.33 0.621 1.12

Matrix: blastn matrix:1 -2  
Gap Penalties: Existence: 5, Extension: 2  
Number of Sequences: 1  
Number of Hits to DB: 1177  
Number of extensions: 44  
Number of successful extensions: 7  
Number of sequences better than 10.0: 1  
Number of HSP's gapped: 5  
Number of HSP's successfully gapped: 5  
Length of query: 3094  
Length of database: 17,886,619,220  
Length adjustment: 27  
Effective length of query: 3067

Effective length of database: 17,886,619,193  
Effective search space: 54858261064931  
Effective search space used: 54858261064931  
X1: 11 (21.1 bits)  
X2: 26 (50.0 bits)  
X3: 26 (50.0 bits)  
S1: 16 (31.5 bits)  
S2: 22 (43.0 bits)